GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:42:23 ; Search time 26.6 Seconds
                                      (without alignments)
                                      933.568 Million cell updates/sec

Title: US-09-483-543A-9
Perfect score: 1733
Sequence: 1 KRGCAGNFDSEERSSWYWGR...........SGCGXGLEVLFQGPVRKGXG 326

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : PIR_68:*
           1: pir1:*
           2: pir2:*
           3: pir3:*
           4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	DB ID	Description
1	1612	93.0	304	2	I58394	c-Crk - mouse
2	1588	91.6	304	2	T27877	hypothetical prote
3	1379.5	79.6	305	1	A45022	CRK-II - human
4	1078	62.2	239	2	A49011	c-Crk - chicken
5	1052	60.7	204	2	A46243	epidermal growth f
6	917.5	52.9	303	2	B45022	CRK-I - human
7	911.5	52.6	303	2	S41754	CRK protein - hum
8	834.5	48.2	259	2	S58352	SH2/SH3 adaptor pr
9	818.	47.2	232	1	A44988	SH2/SH3 adaptor pr
10	236	13.6	211	2	TVFV10	transforming prote
11	224	12.9	217	2	TVHUV	transforming prote
12	224	12.9	217	2	A46444	SH2-SH3 adaptor pr
13	224	12.9	217	2	S26050	growth factor rece
14	218	12.6	217	2	A54688	modular adaptor Gr
15	202	11.7	228	2	A43321	growth factor rece
16	184	10.6	1291	2	JT0664	SH2-SH3 protein se
17	182	10.5	1097	2	S25730	1-phosphatidylinos
18	178	10.3	1290	2	S00696	hypothetical prote
19	177	10.2	1290	2	T31504	1-phosphatidylinos
20	172.5	10.0	839	1	A36466	1-phosphatidylinos
21	170	9.8	816	2	A31317	transforming prote
22	167	9.6	844	1	TVHUV	transforming prote
23	165	9.5	1270	2	T17257	hypothetical prote
24	164	9.5	1196	2	TVMSVV	adaptor protein in
25	161	9.3	1094	2	TVMSVV	SH3-containing pro
26	158.5	9.1	330	2	T13053	dynamin associated
27	154.5	8.9	878	2	JE0376	Grb-2 related adap
28	152.5	8.8	1011	2	I51940	gene VAV2 protein
29	151.5	8.7	334	2	T33836	dynamin associated
30	151	8.7	1168	1	MWAXIC	hypothetical prote
31	151	8.7	443	1	T27877	myosin heavy chain
32	150	8.7	960	1	A39651	hypothetical prote
33	149.5	8.6	639	2	T13151	discs-large tumor
34	148.5	8.6	1113	1	A47106	adapter protein CM
35	148	8.5	290	2	T42526	myosin heavy chain
36	148	8.5	1044	2	S01966	myosin heavy chain
37	146.5	8.5	1038	2	JT0663	hypothetical prote
38	146	8.4	946	2	I38100	GTPase-activating
39	144.5	8.3	1047	2	A40121	ras GTPase-activat
40	143.5	8.3	870	2	B40121	rho-GTPase-activat
41	142	8.2	450	2	A41973	protein-tyrosine k
42	141	8.1	665	2	JC7191	85K c-Cbl-interact
43	139.5	8.0	1236	1	A53970	1-phosphatidylinos
44	139	8.0	359	2	S27788	neutrophil oxidase
45	139	8.0	557	2	A00629	protein-tyrosine k

ALIGNMENTS

RESULT   1

I58394
c-Crk - mouse
C;Crk - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I58394
R;Ogawa, S.; Toyoshima, H.; Kozutsumi, H.; Hagiwara, K.; Sakai, R.; Tanaka, T.; Hiran
Oncogene 9, 1669-1678, 1994
A;Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates ty
A;Reference number: I58394; MUID:94239744
A;Accession: I58394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-304 <RES>
A;Cross-references: GB:S72408; NID:g632866; PIDN:AAB30755.1; PID:g632867
C;Genetics:
A;Gene: c-crk
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;13-118/Domain: SH2 homology <SH2>
F;139-187/Domain: SH3 homology <SH3>

Query Match   93.0%; Score 1612; DB 2; Length 304;
Best Local Similarity   100.0%; Pred. No. 3.9e-113;
Matches 303; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   5 AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 61

Qy   65 INSSGPRPVPPSPAQPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS 124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 INSSGPRPVPPSPAQPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS 121

Qy   125 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFFKGDILRIRDKPEEQWWNAEDSEGKRGM 184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   122 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFFKGDILRIRDKPEEQWWNAEDSEGKRGM 181

Qy   185 IPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYAR 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   182 IPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYAR 241

Qy   245 VIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPDE 304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 VIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPDE 301

Qy   305 DFS 307
          |||
Db   302 DFS 304

RESULT   2

A45022
CRK-II - human
C;Species: Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Jun-2000
C;Accession: A45022
R;Matsuda, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A;Title: Two species of human CRK cDNA encode proteins with distinct biological activiti
A;Reference number: A45022; MUID:92334347
A;Accession: A45022
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-304 <MAT>
A;Cross-references: GB:D10656; NID:g219554; PIDN:BAA01505.1; PID:g219555
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:108769, NCBIP:108770)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;13-118/Domain: SH2 homology #status atypical <SH2>
F;139-187/Domain: SH3 homology <SH3>

Query Match   91.6%;   Score 1588;   DB 2;   Length 304;
Best Local Similarity   98.7%;   Conservative
Matches 299;   Pred No. 2.4e-111;   Mismatches 3;   Indels 0;   Gaps 0;

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Qy    5 AGNFDSEERSSWWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 AGNFDSEERSSWWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 61

Qy   65 INSSGPRPPVPVPSPAQPPGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVARS 124
        |||||||||||:|||||||||||||||||||||||||||||||||||||||||||||:|||
Db   62 INSSGPRPPVPPSPAQPPGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVSRS 121

Qy  125 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM 184
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM 181

Qy  185 IPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYAR 244
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  182 IPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYAR 241

Qy  245 VIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPDE 304
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  242 VIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPDE 301

Qy  305 DFS 307
        |||
Db  302 DFS 304
```

RESULT 3
A49011
c-Crk - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49011
R;Reichman, C.T.; Mayer, B.J.; Keshav, S.; Hanafusa, H.
Cell Growth Differ. 3, 451-460, 1992
A;Title: The product of the cellular crk gene consists primarily of SH2 and SH3 regions.
A;Reference number: A49011; MUID:93041379
A;Accession: A49011
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <REI>
A;Cross-references: GB:L08168; GB:M32398; NID:g212527; PIDN:AAA49001.1; PID:g212528
A;Experimental source: embryo, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:117106, NCBIP:117107)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;13-119/Domain: SH2 homology <SH2>
F;140-188/Domain: SH3 homology <SH3>

Query Match   79.6%;   Score 1379.5;   DB 1;   Length 305;
Best Local Similarity   84.5%;   Pred No. 9e-96;
Matches 257; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

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Qy    5 AGNFDSEERSSWWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
        ||| ||| ||:|||||||||||| |:||||||||:||||||||||||:|||||||:||||||
Db    2 AGQPDSEDRGSWWTWGRLSRGDAVSLLQGQRHGTFLVRDSSTSPGDFVLSVSESSRVSHYI 61

Qy   65 INSSGPRPPVPVPSPAQP-PGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
        :|| || |     |  :|  ||  | |:||||||||||||:|||||||||||||||||||:|
Db   62 VNSLGPAGGRRAGGEGPGCAPGLNPTRFRIGDQEEFDSLPSLLEFYKIHYLDTTTLIEPVSR 121

Qy  124 SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG 183
        ||| ||||||||||:||||||||||||:|||||||||||||||||||||||||||:: |||
Db  122 SRQNSGVILRQEEVEYVRALFDFNGNDDEDLPFKKGDILRIRDKPEEQWWNAEDMDGKRG 181

Qy  184 MIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYA 243
        |||||||||| |: |||||:| |||: ||||||||||||||||||:||||||||||||:||
Db  182 MIPVPYVEKCRPSSASVSTLTGNQDSSHPQPLGGPEPGPYAQPSINTPLPNLQNGPFYA 241

Qy  244 RVIQKRVPNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPD 303
        |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db  242 RVIQKRVPNAYDKTALALEVGELVKVTKINMSGQWEGECNGKRGHFPFTHVRLLDQQNPD 301

Qy  304 EDFS 307
        ||||
Db  302 EDFS 305
```

RESULT 4
A46243
epidermal growth factor-receptor-binding protein GRB-3 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C;Accession: A46243
R;Margolis, B.; Silvennoinen, O.; Comoglio, F.; Roonprapunt, C.; Skolnik, E.; Ullrich
Proc. Natl. Acad. Sci. U.S.A. 89, 8894-8898, 1992
A;Title: High-efficiency expression/cloning of epidermal growth factor-receptor-bindi
A;Reference number: A46243; MUID:93028373
A;Accession: A46243
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-239 <MAR>
A;Note: sequence extracted from NCBI backbone (NCBIP:115326)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: growth factor receptor
F;44-149/Domain: SH2 homology <SH2>
F;170-218/Domain: SH3 homology <SH3>

Query Match   99.5%;   Score 1078;   DB 2;   Length 239;
Best Local Similarity   99.5%;   Pred No. 2.1e-73;
Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    5 AGNFDSEERSSWWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   33 AGNFDSEERSSWWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 92

Qy   65 INSSGPRPPVPVPSPAQPPGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVARS 124
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Db   93 INSSGPRPPVPVPSPAQPPGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVARS 152

Qy  125 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM 184
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  153 RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM 212

Qy  185 IPVPYVEKYRPASASVSALIGGNQEGS 211
        |||||||||||||||||||||||||||
Db  213 IPVPYVEKYRPASASVSALIGGNQEGS 239
```

RESULT 5
B45022
CRK-I - human

```
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 12-Feb-1999
C;Accession: B45022
R;Matsuda, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.
Mol. Cell. Biol. 12, 3482-3489, 1992
A;Title: Two species of human CRK cDNA encode proteins with distinct biological activiti
A;Reference number: A45022; MUID:92334347
A;Accession: B45022
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <MAT>
A;Experimental source: embryonic lung cells
A;Note: sequence extracted from NCBI backbone (NCBIN:108771, NCBIP:108772)
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;13-118/Domain: SH2 homology <SH2>
F;139-187/Domain: SH3 homology <SH3>

Query Match          60.7%;   Score 1052;  DB 2;   Length 204;
Best Local Similarity 99.0%;  Pred. No. 1.5e-71;
Matches  200;  Conservative  1;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    5  AGNFDSEERSSWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI  64
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2  AGNFDSEERSSWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI  61

Qy   65  INSSGPRPEVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS  124
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62  INSSGPRPEVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVSRS  121

Qy  125  RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM  184
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  122  RQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM  181

Qy  185  IPVPYVEKYRPASASVSALIGG  206
            ||||||||||||||||||||||
Db  182  IPVPYVEKYRPASASVSALIGG  203


RESULT 6
S41754
CRKL protein - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S41754
R;ten Hoeve, J.; Morris, C.; Heisterkamp, N.; Groffen, J.
Oncogene 8, 2469-2474, 1993
A;Title: Isolation and chromosomal localization of CRKL, a human crk-like gene.
A;Reference number: S41754; MUID:93368949
A;Accession: S41754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-303 <TEN>
A;Cross-references: EMBL:X59656; NID:g416519; PIDN:CAA42199.1; PID:g416520
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;14-102/Domain: SH2 homology <SH2>
F;130-178/Domain: SH3 homology <SH3>

Query Match          52.9%;   Score 917.5;  DB 2;   Length 303;
Best Local Similarity 56.6%;  Pred. No. 2.7e-61;
Matches  185;  Conservative  33;  Mismatches  56;  Indels  53;  Gaps  6;

Qy    5  AGNFDSEERSSWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI  64
            ||| :||:||| |||| ||||||||  |||||||:||||||| ||||||||||||||||||
Db    3  SARFDSSDRSAWTWGPVSRQEAQTRLQGQRHGMFLVRDSSTCPGDYVLSVSENSRVSHYI  62

Qy   65  INSSGPRPEVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR-  123
            |||
Db   63  INSLPNR------------------------------------------------------ 105

Qy  124  ------SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAED  177
            |||||||||||||||||||||||||||||||
Db  105  RFKIGDQEFDHLPALLEFYKIHYLDTTTLIEPAPRY  105

Db  106  PSPPMGSVSAPNLPTAEDNLEYVRTLYDFPGNDAEDLPFKKGEILVIIEKPEEQWWSARN  165

Qy  178  SEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSH----PQPLGGPEPG-PYAQPSVN--  230
            :|: ||||||||||||||||||||||||  :| |     |||| ||| |    |
Db  166  KDGRVGMIPVPYVEK----------LVRSSPHGKHGNRNSNSYGIPEPAHAYAQPQTTTP  215

Qy  231  --------------TPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKYTKINVSGQW  278
            ||| |:||| ::| |||:|::||| |||||:||||||||||||::||  :|
Db  216  LPAVSGGSPGAAITPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGDIVKVTRMNINGQW  275

Qy  279  EGECNGKRGHFPFTHVRLLDQQNPDED  305
            ||| ||:|| ||||||| | |||||
Db  276  EGEVNGRKGLFPFTHVKIFDPQNPDEN  302


RESULT 7
S58352
SH2/SH3 adaptor protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C;Accession: S58352
R;de Jong, R.; Haataja, L.; Voncken, J.W.; Heisterkamp, N.; Groffen, J.
submitted to the EMBL Data Library, August 1995
A;Description: Tyrosine phosphorylation of murine Crkl.
A;Reference number: S58352
A;Accession: S58352
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-303 <DEJ>
A;Cross-references: EMBL:X90648; NID:g945008; PIDN:CAA62220.1; PID:g945009
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;14-102/Domain: SH2 homology <SH2>
F;130-178/Domain: SH3 homology <SH3>

Query Match          52.6%;   Score 911.5;  DB 2;   Length 303;
Best Local Similarity 56.0%;  Pred. No. 7.7e-61;
Matches  183;  Conservative  34;  Mismatches  57;  Indels  53;  Gaps  6;

Qy    5  AGNFDSEERSSWTWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI  64
            ||| :||:||| |||| ||||||||  |||||||:||||||| ||||||||||||||||||
Db    3  SARFDSSDRSAWTWGPVTRQEAQTRLQGQRHGMFLVRDSSTCPGDYVLSVSENSRVSHYI  62

Qy   65  INSSGPRPEVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR-  123
            |||
Db   63  INSLPNR------------------------------------------------------ 105

Qy  124  ------SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAED  177
            |||||||||||||||||||||||||||||||
Db  105  RFKIGDQEFDHLPALLEFYKIHYLDTTTLIEPAPRY  105

Db  106  PSPPMGSVSAPNLPTAEDNLEYVRTLYDFPGNDAEDLPFKKGEILVIIEKPEEQWWSARN  165

Qy  178  SEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSH----PQPLGGPEPG-PYAQPSVNTP  232
            :|: ||||||||||||||||||||||||  :| |     |||| ||| |    | |
Db  166  KDGRVGMIPVPYVEK----------LVRSSPHGKHGNRNSNSYGIPEPAHAYAQPQTTTP  215

Qy  233  LPNL---------------QNGPIYARVIQKRVPNAYDKTALALEVGELVKINVSGQW  278
            || :                 ||| ||||:||||||||||||::||  :|
Db  216  LPTVASTPGAAINPLPSTQNGPVFAKAIQKRVPCAYDKTALALEVGDIVKVTRMNINGQW  275

Qy  279  EGECNGKRGHFPFTHVRLLDQQNPDED  305
            ||| ||:|| ||||||| | |||||
Db  276  EGEVNGRKGLFPFTHVKIFDPQNPDDN  302


RESULT 8
A44988
transforming protein (gag-crk) - avian sarcoma virus (fragments)
C;Species: avian sarcoma virus
C;Date: 28-Apr-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: A44988
R;Tsuchie, H.; Chang, C.H.W.; Yoshida, M.; Vogt, P.K.
Oncogene 4, 1281-1284, 1989
A;Title: A newly isolated avian sarcoma virus, ASV-1, carries the crk oncogene.
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A;Reference number: A44988; MUID:90045469
A;Accession: A44988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <TSU>
A;Cross-references: GB:X17292
A;Note: the authors translated the codon CGG for residue 79 as Gly, and CAG for residue
C;Superfamily: crk transforming protein; SH2 homology <SH2>
F;67-173/Domain: SH2 homology <SH2>
F;194-242/Domain: SH3 homology <SH3>

Query Match             48.2%;  Score 834.5;  DB 2;  Length 259;
Best Local Similarity   78.3%;  Pred. No. 3.5e-55;
Matches 159;  Conservative 17;  Mismatches 26;  Indels  1;  Gaps  1;

Qy      5 AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVLVRDSSTSPGDYVLSVSENSRVSHYI 64
            ||  |||||| |||||||||||||||:|||| |||||| :|||:||:||||||||||||
Db     56 AGQFDSEDRGSWYWGRLSRGDAVSLLQRERHGTFLVRDSGSIPGDFVLSVSESSRVSHYI 115

Qy     65 INSSGPRPVPPSPAQP-PGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
            :|| ||   |   || ||:| |||:|||||||||||:|||::||||||||||||||:|
Db    116 VNSLGPAGRRAGGEGPGAPGLNPTRFRIGDQEFDSLPSLLEEYKIHYLDTTTLIEPVSR 175

Qy    124 SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG 183
            |||.||||||||| |||||||||.|||:|||||||||||:|||||||||||||||.:||||
Db    176 SRQNSGVILRQEEVEYVRALFDFENGNDDEDLPFKKGDILKIRDKPEEQWWNAEDMDGKRG 235

Qy    184 MIPVPYVEKRPASASVSALIGG 206
            ||||||||||| ||||||:| ||
Db    236 MIPVPYVEKRPSSASVSTLTGG 258


RESULT  9
TVFV10
transforming protein crk - avian sarcoma virus CT10
C;Species: avian sarcoma virus CT10
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 03-Mar-1995
C;Accession: B29851
R;Mayer, B.J.; Hamaguchi, M.; Hanafusa, H.
Nature 332, 272-275, 1988
A;Title: A novel viral oncogene with structural similarity to phospholipase C.
A;Reference number: S00872; MUID:88156964
A;Accession: B29851
A;Molecule type: genomic RNA
A;Residues: 1-232 <MAY>
A;Cross-references: EMBL:Y00302
C;Genetics:
A;Gene: crk
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: transforming protein
F;40-146/Domain: SH2 homology #status atypical <SH2>
F;167-215/Domain: SH3 homology <SH3>

Query Match             47.2%;  Score 818.5;  DB 1;  Length 232;
Best Local Similarity   77.3%;  Pred. No. 4.8e-54;
Matches 157;  Conservative 16;  Mismatches 29;  Indels  1;  Gaps  1;

Qy      5 AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVLVRDSSTSPGDYVLSVSENSRVSHYI 64
            ||  |||||| |||||||||||||||||||| ||||||.|||:|:||||||||||||||
Db     29 AGQFDSEDRGSWYWGRLSRGDAVSLLQGQRHGTPLVRDSGSIPDFVLSVSESSRVSHYI 88

Qy     65 INSSGPRPVPPSPAQP-PGVSFSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
            :|| ||   |   || ||:| |||:||||||:|||||:|||::||||||||||||||:|
Db     89 VNSLGPAGRRAGGEGPGAPGLNPTRFLIGDQVFDSLPSLLEEYKIHYLDTTTLIEPVSR 148

Qy    124 SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG 183
            |||.|||||||||.|||||||||.|||:.|||||||||||:|||||||||:|||||.:||||
Db    149 SRQNSGVILRQEEVEYVRALFDFKGNDDGDLPFKKGDILKIRDKPEEQWNAEDMDGKRG 208

Qy    184 MIPVPYVEKRPASASVSALIGG 206
            ||||||||||| ||||||:| ||
Db    209 MIPVPYVEKRPSSASVSTLTGG 231


RESULT  10
A46444
SH2-SH3 adaptor protein drk - fruit fly (Drosophila melanogaster)
N;Alternate names: gene drk protein
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 03-Dec-1999
C;Accession: A46444; A46443
R;Olivier, J.P.; Raabe, T.; Henkemeyer, M.; Dickson, B.; Mbamalu, G.; Margolis, B.; S
Cell 73, 179-191, 1993
A;Title: A Drosophila SH2-SH3 adaptor protein implicated in coupling the sevenless ty
A;Reference number: A46444; MUID:93214990
A;Accession: A46444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <OLI>
A;Note: sequence extracted from NCBI backbone (NCBIN:128546, NCBIP:128547)
R;Simon, M.A.; Dodson, G.S.; Rubin, G.M.
Cell 73, 169-177, 1993
A;Title: An SH3-SH2-SH3 protein is required for p21Ras1 activation and binds to seven
A;Reference number: A46443; MUID:93214989
A;Accession: A46443
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-211 <SIM>
A;Cross-references: GB:L12446; NID:g304808; PID:g304809
A;Note: sequence extracted from NCBI backbone (NCBIP:128545)
C;Genetics:
A;Gene: drk; E(sev)2B
A;Cross-references: FlyBase:FBgn0004638
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Note: Downstream of Receptor Kinases (drk)
F;5-53/Domain: SH3 homology <SH31>
F;60-149/Domain: SH2 homology <SH2>
F;159-206/Domain: SH3 homology <SH32>

Query Match             13.6%;  Score 236;  DB 2;  Length 211;
Best Local Similarity   29.6%;  Pred. No. 1.3e-10;
Matches 56;  Conservative 37;  Mismatches 64;  Indels 32;  Gaps  5;

Qy      7 NFDSEERSSWYWGRLSRQEAVALLQGQRHGVLVRDSSTSPGDYVLSVSENSRVSHYIIN 66
            |:   . ::|:||||:| :| ||.....|. :||::. .||| :|||.   ::|:|| |
Db     51 NVIEMKNHDWYYGRITRADAEKLLSNKHEGAFLIRISESSPGDFSLSVKCPDGVQHFKVL 110

Qy     67 SSGPRPVPPSPAQPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQ 126
            ..                 :|| :.: ::|.|.::.:: :|:               |
Db    111 RD------------AQSKFFLMVVKPNSLNELVEYHR-------TASVSRSQD 144

Qy    127 GSGVILRQ--EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGM 184
              ...:|:   :.|: :| ||||   :.. ||.:||:| : ||..| ||||  | .|:|
Db    145 --VKLRDMIPEEMLVQALYDFVPQESGELDFRRGDVITVYDRSDENWWNGEIG-NRKGI 200

Qy    185 IPVPYVEKY 193
            .| .|| |
Db    201 FPATYVPY 209


RESULT  11
S26050
growth factor receptor-bound protein, GRB2 - rat
N;Alternate names: Ash-m; Ash-s; gene ash protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S26050; 155429; 170120
R;Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992
A;Title: Cloning of ASH, a ubiquitous protein composed of one Src homology region (SH
A;Reference number: S26050
A;Accession: S26050; MUID:93028395
A;Status: preliminary
```

```
A;Molecule type: mRNA
A;Residues: 1-217 <MAT>
A;Cross-references: EMBL:X62853; NID:g55762; PIDN:CAA44665.1; PID:g55763
R;Watanabe, K.; Fukuchi, T.; Hosoya, H.; Shirasawa, T.; Matuoka, K.; Miki, H.; Takenawa,
J. Biol. Chem. 270, 13733-13739 1995
A;Title: Splicing isoforms of rat Ash/Grb2. Isolation and characterization of the cDNA a
A;Reference number: 155429; MUID:95293967
A;Accession: 155429
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-156,171-217 <RES>
A;Cross-references: GB:D49846; NID:g914956; PIDN:BAA08645.1; PID:g914957
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-59 <RE2>
A;Cross-references: GB:D49847; NID:g914960; PIDN:BAA08646.1; PID:g914961
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: growth factor receptor
F;5-53/Domain: SH3 homology <SH31>
F;60-150/Domain: SH2 homology <SH2>
F;163-210/Domain: SH3 homology <SH32>

Qy    Query Match    12.9%;    Score 224;    DB 2;    Length 217;
Best Local Similarity    27.9%;    Pred. No. 1e-09;
Matches    53;    Conservative    44;    Mismatches    57;    Indels    36;    Gaps    7;

Qy    7  NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
Db   51  NYIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKV 110

Qy   66  NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
Db  111  LRDG-----------------AGKYFLWVVKFNSLNELVDYHR-----STS----VSRNQ 144

Qy  126  QGSGVILRQ--------EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG 180
Db  145  Q---IFLRDIEQVPQQPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGA-CHG 200

Qy  181  KRGMIPVPYV 190
Db  201  QTGMFPRNYV 210


RESULT 12
A54688
modular adaptor Grb2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jan-2000
C;Accession: A54688
R;Suen, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.
Mol. Cell. Biol. 13, 5500-5512, 1993
A;Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2
A;Reference number: A54688; MUID:93360985
A;Accession: A54688
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-217 <SUE>
A;Cross-references: GB:U07617; NID:g464004; PIDN:AAB40022.1; PID:g464005
C;Genetics:
A;Gene: grb2
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: growth factor receptor
F;5-53/Domain: SH3 homology <SH31>
F;60-150/Domain: SH2 homology <SH2>
F;163-210/Domain: SH3 homology <SH32>

Qy    Query Match    12.9%;    Score 224;    DB 2;    Length 217;
Best Local Similarity    27.9%;    Pred. No. 1e-09;
Matches    53;    Conservative    44;    Mismatches    57;    Indels    36;    Gaps    7;

Qy    7  NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
Db   51  NYIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKV 110

Qy   66  NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
```

```
RESULT 13
A43321
growth factor receptor-bound protein 2 - human
N;Alternate names: abundant-src-homology (ash) protein
N;Contains: growth factor receptor-bound protein 3-3
C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A43321; A54064; A46278
R;Lowenstein, E.J.; Daly, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lammers, R.; Ullr
Cell 70, 431-442, 1992
A;Title: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinas
A;Reference number: A43321; MUID:92354060
A;Accession: A43321
A;Molecule type: mRNA
A;Residues: 1-217 <LOW>
A;Cross-references: GB:M96995; NID:g181975; PIDN:AAA58448.1; PID:g181976
A;Note: sequence extracted from NCBI backbone (NCBIN:110294, NCBIP:110295)
R;Fath, I.; Schweighoffer, F.; Rey, I.; Multon, M.C.; Boiziau, J.; Duchesne, M.; Tocq
Science 264, 971-974, 1994
A;Title: Cloning of a Grb2 isoform with apoptotic properties.
A;Reference number: A54064; MUID:94233382
A;Accession: A54064
A;Molecule type: mRNA
A;Residues: 1-59,101-217 <FAT>
A;Cross-references: GB:L29511; NID:g460667; PIDN:AAC37549.1; PID:g498178
R;Matuoka, K.; Shibata, M.; Yamakawa, A.; Takenawa, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992
A;Title: Cloning of ASH, a ubiquitous protein composed of one src homology region (SH
A;Reference number: A46278; S26050; MUID:93028395
A;Accession: A46278
A;Molecule type: mRNA
A;Residues: 58-217 <MAT>
A;Cross-references: EMBL:X62852; NID:g28875; PIDN:CAA44664.1; PID:g28876
C;Genetics:
A;Gene: GDB:GRB2
A;Cross-references: GDB:134732; OMIM:600180
A;Map position: 17q24-17q25
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: alternative splicing; growth factor receptor
F;1-217/Product: growth factor receptor-bound protein 2 #status predicted <LSF>
F;1-59,101-217/Product: growth factor receptor-bound protein 3-3 #status predicted <S
F;5-53/Domain: SH3 homology <SH31>
F;60-150/Domain: SH2 homology <SH2>
F;163-210/Domain: SH3 homology <SH32>

Qy    Query Match    12.9%;    Score 224;    DB 2;    Length 217;
Best Local Similarity    27.9%;    Pred. No. 1e-09;
Matches    53;    Conservative    44;    Mismatches    57;    Indels    36;    Gaps    7;

Qy    7  NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
Db   51  NYIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKV 110

Qy   66  NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
```

```
Db   111 LRDG----------------AGKYFLWVVKFNSLNELVDYHR-----STS----VSRNQ 144
              |  |||  |
Qy   126 QGSGVILRQ-----EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG 180

Db   145 Q---IFLRDIEQVPQQPTYVQALFDDPQEEGELGFRRRGDFIHVMDNSDPNWWKGA-CHG 200

Qy   181 KRGMIPVPYV 190
              | || ||
Db   201 QTGMFPRNYV 210
```

RESULT 14

JT0664
growth factor receptor-binding protein GRB2 homolog - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993
C;Accession: JT0664
R;Wasenius, V.M.; Merilaeinen, J.; Lehto, V.P.
Gene 134, 299-300, 1993
A;Title: Sequence of a chicken cDNA encoding a GRB2 protein.
A;Reference number: JT0664; MUID:94085795
A;Molecule type: mRNA
A;Residues: 1-217 <WAS>
A;Cross-references: GB:L19258; NID:g304385; PIDN:AAA16318.1; PID:g304386
C;Comment: GRB2 protein plays a role in mediating the critical linkage between growth fa
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
C;Keywords: growth factor receptor
F;5-53/Domain: SH3 homology <SH31>
F;60-150/Domain: SH2 homology <SH2>
F;163-210/Domain: SH3 homology <SH32>

```
Qy     7 NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII 65
           :| |:| ::::| |   |  | :| |:   :  ||||  ::|||:|:||:||:|:|:|:
Db    51 NYIEMKPHPWFPGKIPRAKAEEMLGKQRHDGAFLIRESESAPGDFSLSVKFGNDVQQFKV 110

Qy    66 NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
```

Query Match   12.6%; Score 218; DB 2; Length 217;
Best Local Similarity   27.9%; Pred. No. 2.9e-09;
Matches   53; Conservative   44; Mismatches   57; Indels   36; Gaps   7;

A;Reference number: 218361
A;Accession: T15499
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-228 <MIN>
A;Cross-references: EMBL:U29082; NID:g861384; PID:g861389; PIDN:AAA68405.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: sem-5
C;Introns: 26/3; 60/2; 101/2; 137/2; 183/1
C;Superfamily: crk transforming protein; SH2 homology; SH3 homology
F;5-53/Domain: SH3 homology <SH31>
F;60-151/Domain: SH2 homology <SH2>
F;161-208/Domain: SH3 homology <SH32>

Query Match   11.7%; Score 202; DB 2; Length 228;
Best Local Similarity   25.1%; Pred. No. 4.9e-08;
Matches   54; Conservative   39; Mismatches   68; Indels   54; Gaps   6;

```
Qy     7 NFDSEERSSWYWGRLSRQEAVALLQGQ--RHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
           :|:::  :  ||:|:  |:  | :|     :|||:||   :|||:|:|:|:||:|:|:|
Db    51 NVIRMTECNWYLGKITRNDAEVLLKKPTVRDGHFLVRQCESSPGEFSISVRPQDSVQHFK 110

Qy    65 INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQ---------EFDSLPALLEFYKIHYLDTT 115
           :                                       |||| ::||:|||:|||||
Db   111 V----------------------LRDQNGKYILWAVKFNSLNELVAYHRTASVSRT 144

Qy   116 TLIEPVARSRQSSGVILRQE---EAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQW 172
                        :|:||:|    |:|::|||||||: :| :||:|| | :| ||:| |
Db   145 ----------HTILLSDMNVETKEVQALFDFNPQESGELAFKRGDVITLINKDDPNW 191

Qy   173 WNAEDSEGKRGMIPVPYVVEKIRPASASVSALIGGN 207
            | | :  :|:|:|||:||| ||:  :||: | |:
Db   192 WEGQ-LNNRRGIFPSNYVCPYNSNKSNSNVAPGFN 225
```

RESULT 15

S25730
SH2-SH3 protein sem-5 - Caenorhabditis elegans
N;Alternate names: sex-muscle-abnormal protein 5 (sem-5)
C;Species: Caenorhabditis elegans
C;Date: 25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 18-Aug-2000
C;Accession: S25730; T15499
R;Clark, S.G.; Stern, M.J.; Horvitz, H.R.
Nature 356, 340-344, 1992
A;Title: C. elegans cell-signalling gene sem-5 encodes a protein with SH2 and SH3 domain
A;Accession: S25730
A;Molecule type: mRNA
A;Residues: 1-228 <CLA>
A;Status: preliminary
A;Cross-references: GB:S88446; NID:g247604; PID:g247605
R;Minx, P.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C14F5.

Search completed: September 27, 2001, 16:42:24
Job time: 192 sec